## Amendments to the Claims

 (Currently Amended) A method for mapping a gene network comprising the steps of: preparing a plurality of biological samples;

detecting expression of at least five genes in said biological samples;

comparing expression of the at least five genes in a first of said biological samples to expression of the at least five genes in a second of said biological samples;

generating a cluster map for said genes, wherein the cluster map categorizes genes according to similarity in unchanged, increased, or decreased expression <u>levels</u> in the first relative to the second of said biological samples; and

analyzing said cluster map to generate gene network causal models defining regulatory relationships among said genes.

- 2. (Previously Presented) The method of claim 1, wherein absolute amount of transcripts of said genes in each of the biological samples is determined and compared.
- 3. (Original) The method of claim 2, wherein said amount of transcripts is detected with a high density nucleic acid array.
- 4. (Original) The method of claim 1, wherein said biological samples are prepared by a homozygous knockout strategy.
- 5. (Previously Presented) The method of claim 1, wherein each of said biological samples is derived from one clone of cells.

- 6. (Original) The method of claim 1, wherein said biological samples are prepared using cells representing different developmental, physiological or pathological status.
- 7. (Original) The method of claim 1, wherein said biological samples are prepared by stimulating cells with a combination of a plurality of hormones.
- 8. (Original) The method of claim 1, wherein said biological samples are prepared by transfecting cells with a combination of a plurality of vectors, said vectors being used by said cells as templates to transcribe a plurality of RNAs, each of said RNAs having a sequence complementary to one of said genes.
- 9. (Original) The method of claim 1, wherein said gene network causal models are generated and tested using the Linear Structure Relations (LISREL) process performed in a digital computer.

10-105. (Canceled)

- 106. (Currently Amended) The method of claim 7 1 wherein said biological samples are prepared using random chemical mutagenesis.
- 107. (Currently Amended) The method of claim 7 1 wherein said biological samples are prepared using microinjection of antisense RNA or protein into cells.